

Genome Sequences of Three *Leuconostoc citreum* Strains, LBAE C10, LBAE C11, and LBAE E16, Isolated from Wheat Sourdoughs

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***Leuconostoc citreum* is a key microorganism in fermented foods of plant origin. Here we report the draft genome sequence for three strains of *Leuconostoc citreum*, LBAE C10, LBAE C11, and LBAE E16, which have been isolated from traditional French wheat sourdoughs.**

Leuconostoc citreum (formerly *Leuconostoc amelibiosum*) is a heterofermentative lactic acid bacterium that plays an important role in many food fermentations. It has been found in various fermented foods of dairy and plant origins, such as puto, cassava starch, Pozol (a fermented corn beverage), and sourdough (1, 7, 8, 14). *L. citreum* is also described as a key microorganism used as starter for kimchi production, a traditional fermented vegetable food in Korea (5, 6, 10). A complete genome sequence has been reported for strain KM20 isolated from kimchi (9). Furthermore, *L. citreum* is a well-known species that produces α -glucans and β -fructans from sucrose (11, 13). These poly- or oligosaccharides offer large potentialities of industrial uses, such as prebiotic compounds or bulking agents. Linear α -1,6 dextrins are used as blood plasma substitutes, iron transports, or anticoagulant agents and enter in the composition of chromatographic supports, such as Sephadex gels (11, 12, 13). Strains of *L. citreum* are able to produce diverse dextrins and fructans, such as linear α -1,6 dextrins, dextrins with α -(1 \rightarrow 2) ramifications, alternans, and inulin-type fructans (11, 13), and thus appear to be a particularly attractive species. Moreover, antifungal activity of some *L. citreum* strains has been recently reported (15).

L. citreum strains were isolated from wheat traditional French sourdoughs (14); strains LBAE C10 and LBAE C11 were recovered from the same sourdough, and strain LBAE E16 was recovered from another one produced by a different bakery. These strains were found to produce diverse glucans from sucrose containing different amounts of α -(1 \rightarrow 6), α -(1 \rightarrow 3), and α -(1 \rightarrow 2) linkages (2) and exhibited different carbohydrate fermentation and glucanase patterns (3). The genomic DNA of each strain was isolated using the DNeasy blood and tissue kit (Qiagen). The genome was sequenced by a whole-genome shotgun strategy using Roche 454 GS FLX Titanium pyrosequencing. For each genome, the coverage was more than 20-fold (with between 114,132 and 177,078 filtered reads for each strain). Assembly was performed using Newbler 2.5. The draft genome sequences of strains LBAE C10, LBAE C11, and LBAE E16 consisted of 76, 83, and 45 contigs (>100 bp in size), respectively, each comprising 1,934,425 bp, 1,969,963 bp, and 1,801,604 bp. Genome annotation was performed using the AGMIAL annotation platform (4). This resulted in 1,971 (LBAE C10), 2,036 (LBAE C11), and 1,854 (LBAE E16) protein-coding genes, of which 80% (LBAE C10 and LBAE C11)

and 84% (LBAE E16) were annotated with known proteins with biological function and an overall G+C content of around 38.8% for the three strains. Each genome also includes one complete copy of the rRNA operon and 50 (LBAE C10 and LBAE C11), 51 (LBAE E16) tRNA-encoding genes.

Nucleotide sequence accession numbers. The draft genome sequences of *Leuconostoc citreum* LBAE C10, LBAE C11, and LBAE E16 have been deposited in the EMBL nucleotide sequence database under accession no. [CAGE00000000](#), [CAGF00000000](#), and [CAGG00000000](#), respectively.

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